



SEQUENCE LISTING

<110> Hoogenboom Hendricus R.J.M.
Hoogenboom Maria P.G.

<120> MUCIN-1 Specific Binding Members and Methods of Use Thereof

<130> DYX-015.1 US

<140> 09/822,698

<141> 2001-03-30

<150> US 09/538,913

<151> 2000-03-30

<160> 112

<170> Microsoft Word

<210> 1

<211> 113

<212> PRT

<213> artificial sequence

<220>

<223> light chain variable region of the MUC1-specific
binding domain of PH1 Fab antibody

<400> 1

Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

Arg

<210> 2

<211> 339

<212> DNA

<213> artificial sequence

<220>

<223> nucleotide sequence coding for amino acid sequence of
SEQ ID NO:1

<400> 2

gaaattgtgc tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaccta tttggattgg 120
tacctgcaga agccagggca gtctccacag ctctgatct attcgggttc tcatcgggcc 180
tccgggggtcc ctgacagggt cagtggcagt gtatcaggca cagattttac actgagaatc 240
agcagagtgg aggctgagga tgttggagtt tattactgca tgcagggtct acagagtcca 300
ttcactttcg gccctgggac caaagtggat atcaaacga 339

<210> 3

<211> 121

<212> PRT

<213> artificial sequence

<220>

<223> heavy chain variable region of the MUC1-specific
binding domain of the PH1 Fab antibody

<400> 3

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn
20 25 30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 4
 <211> 363
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for amino acid sequence of
 SEQ ID NO:3

<400> 4

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cagggtccagc tgggtgcagtc tgggggagggc ttggtacagc ctgggggggtc cctgagactc      60
tcctgtgcag cctctggatt cacgtttaga agtaacgcca tgggctgggt ccgccaggct      120
ccaggggaagg ggctggagtg ggtctcaggt attagtggta gtgggtggcag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgag agccgaggac acggccgtat attattgtgc gaaacatacc      300
ggggggggcg tttgggaccc cattgactac tggggccagg gaaccctggc caccgtctca      360
agc                                                                    363
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<210> 5
 <211> 381
 <212> PRT
 <213> artificial sequence

<220>
 <223> MUC1-specific immunocytokine bivPH1-IL-2

<400> 5

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn
20          25          30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35          40          45
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65          70          75          80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85          90          95
Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
100         105         110
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Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ala Leu Glu Ile
 115 120 125
 Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro
 130 135 140
 Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly
 145 150 155 160
 Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln
 165 170 175
 Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro Asp Arg
 180 185 190
 Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg
 195 200 205
 Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Leu Gln
 210 215 220
 Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Gly
 225 230 235 240
 Gly Gly Ser Gly Gly Gly Ala Leu Ala Pro Thr Ser Ser Ser Thr Lys
 245 250 255
 Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile
 260 265 270
 Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu
 275 280 285
 Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu
 290 295 300
 Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu
 305 310 315 320
 Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn
 325 330 335
 Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met
 340 345 350
 Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg
 355 360 365
 Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
 370 375 380

<210> 6
 <211> 1143
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for amino acid sequence of
 SEQ ID NO:5

<400> 6

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tcctgtgcag cctctggatt cacgtttaga agtaacgccca tgggctgggt ccgccagget	120
ccaggggaagg ggctggagtg ggtctcaggt attagtggta gtggtggcag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaataga acagcctgag agccgaggac acggccgtat attattgtgc gaaacatacc	300
ggggggggcg tttgggaccc cattgactac tggggccagg gaaccctggg caccgtctca	360
agcggaggcg gtgcacttga aattgtgctg actcagtcct cactctccct gcccgtcacc	420
cctggagagc cggcctccat ctctgcagg tctagtcaga gcctcctgca tagtaatgga	480
tacacctatt tggattggta cctgcagaag ccagggcagt ctccacagct cctgatctat	540
tcgggttctc atcgggcctc cggggtcctt gacaggttca gtggcagtg atcaggcaca	600
gattttacac tgagaatcag cagagtggag gctgaggatg ttggagtta ttactgcatg	660
cagggctctac agagtccatt cactttcggc cctgggacca aagtggatat caaacgaggg	720
ggtggatcag gcggcggggc cctagcacct acttcaagtt ctacaaagaa aacacagcta	780
caactggagc atttactgct ggatttacag atgattttga atggaattaa taattacaag	840
aatcccaaac tcaccaggat gctcacattt aagttttaca tgcccaagaa ggccacagaa	900
ctgaaacatc ttcagtgtct agaagaagaa ctcaaacctc tggaggaagt gctaaattta	960
gctcaaagca aaaactttca cttaagacct agggacttaa tcagcaatat caacgtaata	1020
gttctggaac taaagggatc tgaaacaaca ttcatgtgtg aatatgctga tgagacagca	1080
accattgtag aatttctgaa cagatggatt acctttgtc aaagcatcat ctcaacactg	1140
act	1143

<210> 7
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> peptide of MUC1 protein

<400> 7

Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly
 1 5 10 15
 Ser Thr Ala Pro
 20

<210> 8
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> peptide of MUC1 protein

<400> 8

Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro
 1 5 10 15

Pro Ala His Gly
 20

<210> 9
 <211> 24
 <212> DNA
 <213> artificial sequence

<220>
 <223> CH1FOR primer

<400> 9

gtccttgacc aggcagccca gggc 24

<210> 10
 <211> 23
 <212> DNA
 <213> artificial sequence

<220>
 <223> pUC-reverse primer

<400> 10

agcggataac aatttcacac agg 23

<210> 11
 <211> 44
 <212> DNA
 <213> artificial sequence

<220>
 <223> VL backward primer

<400> 11

accgcctcca ccagtgcact tgaaattgtg ctgactcagt ctcc 44

<210> 12

<211> 51

<212> DNA

<213> artificial sequence

<220>

<223> VL forward primer

<400> 12

accgcctcca ccgggcgcg cttattaaca ctctcccctg ttgaagctct t 51

<210> 13

<211> 61

<212> DNA

<213> artificial sequence

<220>

<223> VL backward primer for light chain variable region
of the PH1 Fab antibody with additional linker and
restriction sites

<400> 13

gccgatcgct ctggtcaccg tctcaagcgg aggcggtgca cttgaaattg tgctgactca 60

g 61

<210> 14

<211> 50

<212> DNA

<213> artificial sequence

<220>

<223> VL forward primer for light chain variable region
of PH1 Fab antibody with additional linker and
restriction sites

<400> 14

gtctcgcgag cggccgccga ttggatatcc actttgggtcc cagggccgaa 50

<210> 15

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> nucleotide sequence coding for a

nine amino acid linker

<400> 15

gggggtggat caggcggcgg ggccta

27

<210> 16

<211> 69

<212> DNA

<213> artificial sequence

<220>

<223> PH1-IL-2 backward primer

<400> 16

accaaagtgg atatcaaacg aggggggtgga tcaggcggcg gggccctagc acctacttca

60

agttctaca

69

<210> 17

<211> 49

<212> DNA

<213> artificial sequence

<220>

<223> PH1-IL-2 forward primer

<400> 17

gtcccgcgtg cggccgcagt cagtgttgag atgatgcttt gacaaaagg

49

<210> 18

<211> 98

<212> PRT

<213> artificial sequence

<220>

<223> heavy chain variable region from a DP47 germ line

<400> 18

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys

<210> 19
<211> 100
<212> PRT
<213> artificial sequence

<220>
<223> light chain variable region from a DPK 15 germ line

<400> 19

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Leu Gln Thr Pro
100

<210> 20
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> myc tag peptide

<400> 20

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
1 5 10

<210> 21
<211> 42

<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for amino acid sequence
of SEQ ID NO:20

<400> 21

gaacaaaaac tcatctcaga agaggatctg aatggggccg ca

42

<210> 22
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> hexahistidine peptide

<400> 22

His His His His His His
1 5

<210> 23
<211> 18
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for amino acid sequence
of SEQ ID NO:22

<400> 23

catcaccatc atcaccat

18

<210> 24
<211> 220
<212> PRT
<213> artificial sequence

<220>
<223> immunoglobulin kappa light chain of MUC1-specific PH1-IgG1

<400> 24

Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35										40										45										
Pro	Gln	Leu	Leu	Ile	Tyr	Ser	Gly	Ser	His	Arg	Ala	Ser	Gly	Val	Pro															
50						55					60																			
Asp	Arg	Phe	Ser	Gly	Ser	Val	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Arg	Ile															
65					70					75					80															
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Gly															
			85					90						95																
Leu	Gln	Ser	Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys															
			100					105						110																
Arg	Gly	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp															
			115				120							125																
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn															
			130				135							140																
Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu															
			145			150				155					160															
Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp															
			165					170						175																
Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr															
			180					185						190																
Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser															
			195				200							205																
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys																			
			210			215					220																			

<210> 25
 <211> 663
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for amino acid sequence of
 SEQ ID NO:24

<400> 25

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tacctgcaga	agccagggca	gtctccacag	ctcctgatct	attcgggttc	tcatcgggcc	180
tccggggtcc	ctgacagggt	cagtggcagt	gtatcaggca	cagattttac	actgagaatc	240
agcagagtgg	aggctgagga	tgttggagtt	tattactgca	tgcagggtct	acagagtcca	300

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ttcacttttcg gccctgggac caaagtggat atcaaacgag gaactgtggc tgcaccatct 360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttggtgtgc 420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccttc 480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600
gaagtcaccc atcagggcct gagttcaccg gtgacaaaaga gcttcaacag gggagagtgt 660
tag 663

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<210> 26
<211> 451
<212> PRT
<213> artificial sequence

<220>
<223> immunoglobulin heavy chain of MUC1-specific PH1-IgG1

<400> 26

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn
          20          25          30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
          50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
          65          70          75          80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
          100          105          110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
          115          120          125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
          130          135          140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
          145          150          155          160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
          165          170          175

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Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val		
			180					185					190				
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His		
		195					200					205					
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys		
	210					215					220						
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly		
225					230					235					240		
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met		
			245						250						255		
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His		
			260					265					270				
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val		
	275						280					285					
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr		
	290					295					300						
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly		
305					310					315					320		
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile		
			325					330					335				
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val		
			340					345					350				
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser		
	355					360						365					
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu		
	370					375					380						
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro		
385					390					395					400		
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val		
			405						410					415			
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met		
		420						425					430				
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser		
	435						440					445					
Pro	Gly	Lys															
	450																

<210> 27

<211> 1356
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for amino acid sequence of
 SEQ ID NO:26

<400> 27

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ccaggggaagg ggctggagtg ggtctcaggt attagtggta gtgggtggcag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgag agccgaggac acggccgtat attattgtgc gaaacatacc	300
gggggggggcg tttgggaccc cattgactac tggggccagg gaaccctggc caccgtctca	360
agcgccctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct	420
gggggacacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtccacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtagtg accgtgccct ccagcagctt gggcaccacg	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca cctcatgat ctcccggacc	780
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tgggtacgtg acggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggc ctccaacaaa gccctcccag ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat	1080
gagctgacca agaaccaggc cagcctgacc tgcctgggtc aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc	1200
gtgctggact ccgacggctc cttcttcttc tacagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctcctt aagtcgggga aaataa	1356

<210> 28
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <221> variant
 <222> (1)..(14)
 <223> amino acid positions designated Xaa may be varied
 to form alternative regions of a MUC1-specific
 binding member as explained in the disclosure

 <400> 28

Xaa Xaa His Thr Gly Xaa Gly Val Trp Xaa Pro Xaa Xaa Xaa
 1 5 10

<210> 29
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 29

Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Gly Tyr
 1 5 10

<210> 30
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 30

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys His
 1 5 10

<210> 31
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 31

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr

1

5

10

<210> 32
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> amino acid sequence in a MUC1-specific binding member

 <400> 32

Ala Ile His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys Tyr
 1 5 10

<210> 33
 <211> 33
 <212> DNA
 <213> artificial sequence

 <220>
 <221> misc_feature
 <222> (1)..(33)
 <223> n may be varied according to the disclosure
 to form mutagenic primer sequences

 <400> 33
 ggattcacgt ttagannnaa cgccatgggc tgg

33

<210> 34
 <211> 39
 <212> DNA
 <213> artificial sequence

 <220>
 <221> misc_feature
 <222> (1)..(39)
 <223> n may be varied according to the disclosure
 to form mutagenic primer sequences

 <400> 34

cacggagtct gcgtannntg tnnngccacc actaccact

39

<210> 35
 <211> 90
 <212> DNA
 <213> artificial sequence

 <220>
 <221> misc_feature
 <222> (1)..(90)

<210> 39
<211> 56
<212> DNA
<213> artificial sequence

<220>
<223> VH1c back Sfi primer

<400> 39

gtcctcgcaa ctgcgggcca gccggccatg gccsaggtcc agctggtrca gtctgg 56

<210> 40
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> PAP peptide epitope of MUC1 bound by PH1 Fab antibody

<400> 40

Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala Leu
1 5 10 15

<210> 41
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 41

Ala Lys His Asn Thr Ser Lys Val Trp Asp Pro Ile Asp Tyr Trp Gly
1 5 10 15

<210> 42
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for a mutant CDR3 region

<400> 42

gcgaaacata atacgtctaa ggtttgggac cccattgact actggggc 48

<210> 43

<211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 43

Ala Lys Ser Ser Thr Thr Thr Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 44
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 44

gcgaaatcta gtactacgac ggtttgggac cccattgact actggggc

48

<210> 45
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <221> variant
 <222> (1)..(16)
 <223> Xaa, designated as "&" in the disclosure, indicates end
 of amino acid sequence because mutation in nucleotide
 sequence forms a translational stop codon

<400> 45

Ala Lys Xaa Pro Met Ala Asn Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 46
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 46

gcgaaatagc ctatggcgaa tgtttgggac cccattgact actggggc

48

<210> 47
 <211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <221> variant
 <222> (1)..(16)
 <223> Xaa, designated as "&" in the disclosure, indicates end
 of amino acid sequence because mutation in nucleotide
 sequence forms a translational stop codon

 <400> 47

 Ala Lys Xaa His Thr Lys Thr Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 48
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 48

gcgaaatagc atacgaagac ggtttgggac cccattgact actggggc 48

<210> 49
 <211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 49

Ala Lys Ile Thr Val Ser Arg Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 50
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 50

gcgaaaatta ctgttagtcg tgtttgggac cccattgact actggggc 48

<210> 51
 <211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 51

Ala	Lys	Arg	Tyr	Leu	Tyr	Asp	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 52
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 52

gcgaaacgtt atctgtatga tgtttgggac cccattgact actggggc 48

<210> 53
 <211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 53

Ala	Lys	His	Thr	Gly	Gly	Gly	Thr	Leu	Gln	Arg	Leu	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 54
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 54

gcgaaacata ccgggggggg cactttgcag cggttgact actggggc 48

<210> 55
 <211> 16

<212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 55

Ala	Lys	His	Thr	Gly	Gly	Gly	Thr	Gln	Thr	Pro	Cys	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 56
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 56

gcgaaacata ccggggggggg cactcagact ccgtgtgact actggggc 48

<210> 57
 <211> 16
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 57

Ala	Lys	His	Thr	Gly	Gly	Gly	Arg	Arg	Ile	Cys	His	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 58
 <211> 48
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for a mutant CDR3 region

 <400> 58

gcgaaacata ccggggggggg ccgtcgtatt tgtcatgact actggggc 48

<210> 59
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <221> variant
 <222> (1)..(16)
 <223> Xaa, designated as "&" in the disclosure, indicates end
 of amino acid sequence because mutation in nucleotide
 sequence forms a translational stop codon

<400> 59

Ala	Lys	His	Thr	Gly	Gly	Gly	Xaa	Arg	Xaa	Xaa	Arg	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 60
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 60

gcgaaacata ccgggggggg ctagcggtag tagcgggact actggggc

48

<210> 61
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavychain variable region

<400> 61

Ala	Lys	His	Thr	Gly	Gly	Gly	Gln	Lys	Leu	Gln	Leu	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 62
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 62

gcgaaacata ccgggggggg ccagaagctg cagctggact actggggc

48

<210> 63
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <221> variant
 <222> (1)..(16)
 <223> Xaa, when designated as "&" in the disclosure, indicates end of amino acid sequence because mutation in nucleotide sequence forms a translational stop codon; or when designated as "s" in the disclosure, Xaa is serine

<400> 63

Ala	Xaa	His	Thr	Gly	Gly	Arg	Gly	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 64
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 64

gcgtsacata cggggggggcg cggttgggac cccattgact actggggc 48

<210> 65
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 65

Ala	Asn	Gln	Thr	Gly	Gly	Gly	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 66
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 66

gcgaaccaga ctggggggggg cgtttgggac cccattgact actggggc 48

<210> 67
 <211> 16

<212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 67

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr Trp Gly
 1 5 10 15

<210> 68
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 68

gcgagacata ccggtggggg cgtktgggat cccatatact actggggc

48

<210> 69
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 69

Ala Lys Pro Thr Gly Gly Gly Ala Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 70
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 70

gcgaaacctt ccgggggggg cgcttgggac cccattgact actggggc

48

<210> 71
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 71

Ala Lys His Thr Gly Val Gly Val Trp His Pro Ile Tyr Tyr Trp Gly
1 5 10 15

<210> 72
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for a mutant CDR3 region

<400> 72

gcgaaacata ccgggggtggg cgtttggcac cccatctact actgggggc 48

<210> 73
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 73

Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Ile Lys Tyr
1 5 10

<210> 74
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 74

Ala Lys His Thr Gly Glu Gly Val Trp Asp Pro Ile Lys Tyr
1 5 10

<210> 75
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 75

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Lys
1 5 10

<210> 76

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 76

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
1 5 10

<210> 77

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 77

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
1 5 10

<210> 78

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 78

Ser Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
1 5 10

<210> 79

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 79

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly His
1 5 10

<210> 80

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 80

Ala Lys His Thr Gly Gly Gly Val Trp Asn Pro Ile Gly His
1 5 10

<210> 81

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 81

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Leu Gly Tyr
1 5 10

<210> 82

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 82

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Leu Asp Asn
1 5 10

<210> 83

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 83

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr
1 5 10

<210> 84

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 84

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr
1 5 10

<210> 85

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 85

Ala Lys His Thr Gly Ser Gly Val Trp Asp Pro Ile Asn Tyr
1 5 10

<210> 86

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 86

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Asp
1 5 10

<210> 87

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 87

Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Met Asn Tyr
 1 5 10

<210> 88
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 88

Thr Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr
 1 5 10

<210> 89
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 89

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr
 1 5 10

<210> 90
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 90

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Asn
 1 5 10

<210> 91
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 91

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Phe Ala Tyr

1 5 10

<210> 92
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 92

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Ala Ser
1 5 10

<210> 93
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 93

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Asp Tyr
1 5 10

<210> 94
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 94

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile His Tyr
1 5 10

<210> 95
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 95

Ala Ile His Thr Gly Ala Gly Val Trp Asp Pro Ile Arg Tyr
1 5 10

<210> 96
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 96

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ser Ser
 1 5 10

<210> 97
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 97

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Asp
 1 5 10

<210> 98
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 98

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Tyr
 1 5 10

<210> 99
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 99

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Val Asp Tyr
 1 5 10

<210> 100
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 100

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Pro
 1 5 10

<210> 101
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 101

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr
 1 5 10

<210> 102
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 102

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile His Asn
 1 5 10

<210> 103
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

 <400> 103

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met His Tyr
 1 5 10

<210> 104
 <211> 14

<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 104

Ala Lys His Thr Gly Gly Gly Val Trp Asn Pro Ile Asp Tyr
1 5 10

<210> 105
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 105

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr
1 5 10

<210> 106
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 106

Ala Lys His Thr Gly Ala Gly Val Trp Asp Pro Ile Asp Tyr
1 5 10

<210> 107
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 107

Ala Gln His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
1 5 10

<210> 108
<211> 14
<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 108

Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Asp Tyr
1 5 10

<210> 109

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 109

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr
1 5 10

<210> 110

<211> 66

<212> DNA

<213> artificial sequence

<220>

<223> VH1C Back eukaryotic primer

<400> 110

ggactagtc tggagtgcgc gcactcccag gtccagctgg tgcagtctgg gggaggcttg 60

gtacag 66

<210> 111

<211> 73

<212> DNA

<213> artificial sequence

<220>

<223> VKexpress-MUC-for primer

<400> 111

gcgctcgcat ttgcctgtta attaagttag atctattcta ctacggttg atatccactt 60

tggtcccagg gcc 73

<210> 112

<211> 35

<212> DNA

<213> artificial sequence

<220>

<223> MUC1-VL-Back-APA primer

<400> 112

ccagtgcact ccgaaattgt gctgactcag tctcc

35

[illegible]